SEQUENCE LISTING

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MEEK, THOMAS D.
POWELL, DAVID J.
TEW, DAVID G.

<120> Method of Site Specific Labeling of Proteins and Uses Therefor

<130> P50892

<140> 09/889,344
<141> 2001-07-16

<150> PCT/US00/01481
<151> 2000-01-20

<150> US 60/117,327
<151> 1999-01-22

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<210> 1
<211> 5
<212> PRT
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<220>
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<223> Where Xaa at position (5) can represent Leucine or Isoleucine

<220>
<223> Wherein the amino acid sequence is modified by reacting a

<223> transglutaminase with a detectable labeling compound

<400> 1

Gln Ser Lys Val Xaa
1 5

<210> 2

<211> 207

<212> PRT

<213> Artificial Sequence

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<221> unsure

<222> (1)(2)(3)(4)(5)(6)(7)(8)(9)(10)(11)(12)(13)(14)(15)

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<223> Where Xaa can represent none or any one of the twenty naturally

<223> occurring amino acids

<220>

<223> Wherein the amino acid sequence is modified by reacting a

<223> transglutaminase with a detectable labeling compound

<400> 2

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
50 55 60
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65 70 75 80
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
85 90 95
Xaa Xaa Xaa Xaa Xaa Gln Ser Lys Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa
100 105 110
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
115 120 125
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
130 135 140
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
145 150 155 160
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
165 170 175
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
180 185 190
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
195 200 205

<210> 3
<211> 207
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<223> Where Xaa can represent none or any one of the twenty naturally
<223> occurring amino acids

<220>
<223> Wherein the amino acid sequence is modified by reacting a
<223> transglutaminase with a detectable labeling compound

<400> 3

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
50 55 60
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65 70 75 80
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
85 90 95
Xaa Xaa Xaa Xaa Xaa Gln Ser Lys Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa
100 105 110
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
115 120 125
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
130 135 140
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
145 150 155 160
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
165 170 175

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
180 185 190
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
195 200 205

<210> 4
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Derivative of a factor XIII substrate

<400> 4
Leu Ser Leu Ser Gln Ser Lys Val Leu Gly
1 5 10

<210> 5
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Derivative of a factor XIII substrate

<400> 5
Ile Gly Glu Gly Gln Ser Lys Val Leu Gly
1 5 10

<210> 6
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Derivative of a factor XIII substrate

<400> 6
Leu Gly Pro Gly Gln Ser Lys Val Ile Gly
1 5 10

<210> 7
<211> 81
<212> DNA
<213> Unknown

<220>
<223> Oligonucleotide designed to introduce Q tag

<400> 7
tgtacctcag accatatgag cctgtccctg tcccagtcca aagttctgcc gggtccgagc 60
actatcgaag aacgcgttaa g 81

<210> 8
<211> 37
<212> DNA
<213> Unknown

<220>
<223> Oligonucleotide designed to introduce Q tag

<400> 8
tgatgtcagt caagcttacg cctggtggcc gttgatg 37

<210> 9
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Derivative of a factor XIII substrate

<400> 9
Met Ser Leu Ser Leu Ser Gln Ser Lys Val Leu Pro Gly Pro
1 5 10

<210> 10
<211> 37
<212> DNA
<213> Unknown

<220>
<223> Oligonucleotide designed to introduce Q tag

<400> 10
tgtacctcag accatatgag cactatcgaa gaacgcg 37

<210> 11
<211> 78
<212> DNA
<213> Unknown

<220>
<223> Oligonucleotide designed to introduce Q tag

<400> 11
tgatgtcagt caagcttacg gacccggcag aactttggac tgggacaggg acagcgcctg 60
gtggccgttg atgtaatc 78

<210> 12
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Derivative of E. coli ACP protein

<400> 12
Leu Ser Leu Ser Gln Ser Lys Val Leu Pro Gly Pro
1 5 10

<210> 13
<211> 92
<212> DNA
<213> Unknown

<220>
<223> Oligonucleotide designed to introduce Q tag into
Streptococcus haemophilus FabH gene

<400> 13
tatcatatga gcctgtccct gtcccagtcc aaagttctgc cgggtccggg taccctcgag 60
ggatccgctt ttgcaaaaat aagtcaggtt gc 92

<210> 14
<211> 53
<212> DNA
<213> Unknown

<220>
<223> Oligonucleotide designed to introduce Q tag into
Streptococcus haemophilus FabH gene

<400> 14
ctcagatctg agctcactag tggatcctta aattgtaaga atgagcgtgc ccc 53

<210> 15
<211> 364
<212> PRT
<213> Artificial Sequence

<220>
<223> Modified sequence of Streptococus haemophilus FabH

<400> 15

Met	Gly	His	His	His	His	His	His	His	His	His	Ser	Ser	Gly	His
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Ile	Glu	Gly	Arg	His	Met	Ser	Leu	Ser	Leu	Ser	Gln	Ser	Lys	Val	Leu
		20					25					30		
Pro	Gly	Pro	Gly	Thr	Leu	Glu	Gly	Ser	Ala	Phe	Ala	Lys	Ile	Ser	Gln
	35					40					45			
Val	Ala	His	Tyr	Val	Pro	Glu	Gln	Val	Val	Thr	Asn	His	Asp	Leu	Ala
50					55					60					
Gln	Ile	Met	Asp	Thr	Asn	Asp	Glu	Trp	Ile	Ser	Ser	Arg	Thr	Gly	Ile
65				70					75						80
Arg	Gln	Arg	His	Ile	Ser	Arg	Thr	Glu	Ser	Thr	Ser	Asp	Leu	Ala	Thr
			85					90					95		
Glu	Val	Ala	Lys	Lys	Leu	Met	Ala	Lys	Ala	Gly	Ile	Thr	Gly	Lys	Glu
		100					105					110			

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Leu Asp Phe Ile Ile Leu Ala Thr Ile Thr Pro Asp Ser Met Met Pro
        115                 120                 125
Ser Thr Ala Ala Arg Val Gln Ala Asn Ile Gly Ala Asn Lys Ala Phe
    130                 135                 140
Ala Phe Asp Leu Thr Ala Ala Cys Ser Gly Phe Val Phe Ala Leu Ser
145                 150                 155                 160
Thr Ala Glu Lys Phe Ile Ala Ser Gly Arg Phe Gln Lys Gly Leu Val
                165                 170                 175
Ile Gly Ser Glu Thr Leu Ser Lys Ala Val Asp Trp Ser Asp Arg Ser
            180                 185                 190
Thr Ala Val Leu Phe Gly Asp Gly Ala Gly Gly Val Leu Leu Glu Ala
        195                 200                 205
Ser Glu Gln Glu His Phe Leu Ala Glu Ser Leu Asn Ser Asp Gly Ser
    210                 215                 220
Arg Ser Glu Cys Leu Thr Tyr Gly His Ser Gly Leu His Ser Pro Phe
225                 230                 235                 240
Ser Asp Gln Glu Ser Ala Asp Ser Phe Leu Lys Met Asp Gly Arg Thr
                245                 250                 255
Val Phe Asp Phe Ala Ile Arg Asp Val Ala Lys Ser Ile Lys Gln Thr
            260                 265                 270
Ile Asp Glu Ser Pro Ile Glu Val Thr Asp Leu Asp Tyr Leu Leu Leu
        275                 280                 285
His Gln Ala Asn Asp Arg Ile Leu Asp Lys Met Ala Arg Lys Ile Gly
    290                 295                 300
Val Asp Arg Ala Lys Leu Pro Ala Asn Met Met Glu Tyr Gly Asn Thr
305                 310                 315                 320
Ser Ala Ala Ser Ile Pro Ile Leu Leu Ser Glu Cys Val Glu Gln Gly
                325                 330                 335
Leu Ile Pro Leu Asp Gly Ser Gln Thr Val Leu Leu Ser Gly Phe Gly
            340                 345                 350
Gly Gly Leu Thr Trp Gly Thr Leu Ile Leu Thr Ile
        355                 360
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<210> 16
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<213> Artificial Sequence

<220>
<223> Modified sequence of Erythropoietin receptor

fusion protein

<400> 16

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            20                  25                  30
Pro Lys Phe Glu Ser Lys Ala Ala Leu Leu Ala Ala Arg Gly Pro Glu
        35                  40                  45
Glu Leu Leu Cys Phe Thr Glu Arg Leu Glu Asp Leu Val Cys Phe Trp
    50                  55                  60
Glu Glu Ala Ala Ser Ala Gly Val Gly Pro Gly Asn Tyr Ser Phe Ser
65                  70                  75                  80
Tyr Gln Leu Glu Asp Glu Pro Trp Lys Leu Cys Arg Leu His Gln Ala
                85                  90                  95
Pro Thr Ala Arg Gly Ala Val Arg Phe Trp Cys Ser Leu Pro Thr Ala
            100                 105                 110
Asp Thr Ser Ser Phe Val Pro Leu Glu Leu Arg Val Thr Ala Ala Ser
        115                 120                 125
Gly Ala Pro Arg Tyr His Arg Val Ile His Ile Asn Glu Val Val Leu
    130                 135                 140
Leu Asp Ala Pro Val Gly Leu Val Ala Arg Leu Ala Asp Glu Ser Gly
145                 150                 155                 160
His Val Val Leu Arg Trp Leu Pro Pro Pro Glu Thr Pro Met Thr Ser
                165                 170                 175
His Ile Arg Tyr Glu Val Asp Val Ser Ala Gly Asn Gly Ala Gly Ser
            180                 185                 190
Val Gln Arg Val Glu Ile Leu Glu Gly Arg Thr Glu Cys Val Leu Ser
        195                 200                 205
Asn Leu Arg Gly Arg Thr Arg Tyr Thr Phe Ala Val Arg Ala Arg Met
    210                 215                 220
Ala Glu Pro Ser Phe Gly Gly Phe Trp Ser Ala Trp Ser Glu Pro Val
225                 230                 235                 240
Ser Leu Leu Thr Pro Ser Asp Leu Asp Pro Leu Ser Leu Ser Gln Ser
                245                 250                 255
Lys Val Leu Gly Val Phe Phe Ala Glu Ile Glu Gly Arg Gly Thr Glu
            260                 265                 270
Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
        275                 280                 285
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Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
    290                 295                 300
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
305                 310                 315                 320
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
                325                 330                 335
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
            340                 345                 350
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
        355                 360                 365
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
    370                 375                 380
Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
385                 390                 395                 400
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
                405                 410                 415
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
            420                 425                 430
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
        435                 440                 445
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
    450                 455                 460
Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
465                 470                 475                 480
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
                485                 490                 495
Leu Ser Leu Ser Pro Gly Lys
            500
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